

Docket No.: 381552004800

SEQ ID NO:1

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ATG GCT CCC CCG ACA GCC GGC CCC CTT CCT
↑SEQ ID NO:3→

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AGC GCC AAC ATT CTG CCC GTG GTG GAG CCG TGG TGG
M V K L R G G S K G L F V G G C T T C Y Y L D E H
CAC

ATG GTG AAG CTG CGT GGC GGC TCC AAG GGC CTG GTC GGC
R S C I R W R P S R K N E A K I S I D
GAC

CGC TCC TGC ATC CGC TGG AGG CCC TCA CGC AAG AAC GAG TGC GGC
S I O E V S E G R Q S E V F F C C C R Y P D G

TCC ATC CAG GAG GTG AGT GAG GGG CGG CAG TCG GAG GTC TTC GGC GGT
S E D P N C C F S I Y H G S H R C E A G S L D

AGC TTC GAC CCC AAC TGC TGC TTC AGC ATC TAC CAC GGC AGC CAC CCC GAC TTT
C M C T C S E V A R T W V T G L R Y L M

CTG GTC TCC ACC AGC AGC GAG GTG GCG CGC ACC TGG GTC ACT GGC CTG CSC TMS GTC

GCC GGC ATC AGC GAC GAG GAC AGC CTG GCT CGC CGC CAG CGC ACC AGG GAC CAG TCC CTC

AAG CAG ACG TTT GAC GAG GCC GAC AAG AAC GGG GAT GGC AGC CTG AGC ATT GGC GAG GTT

CTG CAG CTG CTG CAC AAG CTC AAC GTG AAC CTG CCC CGG CAG AGG GTG AAG CAG ATG TTG

R E A D T D D H Q G A P CTG GGT TTT GAA GAG TTC TGT GCC TTG

AGG GAA GCG GAC ACG GAT GAC CAC CAA GGG ACG TTT TTT TTT TTT TTT TTT TTT

Y K M M S T R R D L Y L C C T C T G C T G A C C T A C A G C A A C C A
T A C A A G A T G A T G T C C A C C C G C C G G G A C C T C T A C C T G C T C C A T G C T G A C C T A C A G C A A C C A

K D H L D A A S L Q R F L Q GTG GAG CAG AAG ATG GC
AAG GAC CAC CTG GAT GCC GCC AGC CTG CAG CGC TTC CTG CAG

G V T L E S C Q D I I E Q F E C TGC CCA GAA AA
GGT GTG ACC CTC GAG AGC TGC CAG GAC ATC ATC GAG CAG TTT GAG CCA TGC CCA GAA AA

K S K G L L G I D G F T N Y T R S A K A
AAG AGT AAG GGG CTG CTG GGC ATT GAT GGC TTC ACC AAC TAC ACC AGG AGC CCT GCT GG

D I F N P E H H H V H Q D M T Q P L S C A
GAC ATC TTC AAC CCT GAG CAC CAC CAT GTG CAC CAG GAC ATG ACG CAG CCG CTG AGC CA

Y F I T S S H N T Y L V G D Q L M S Q S
TAC TTC ATC ACC TCG TCC CAC AAC ACC TAC CTC GTG GGT GAC CAG CTC ATG TCC CAG TC

CGG GTG GAC ATG TAT GCT TGG GTC CTG CAG GCT GGC TGC CGC TGC GTG GAG GTG GAC TGC

W D G P D G E P I V H H G Y T L T S K I
TGG CAT GGG CCC GAC GGG GAG CCC ATT GTG CAC CAT GGC TAC ACT CTG ACT TCC AAG AT

FIGURE 1a

Title: 32544, A NOVEL HUMAN PHOSPHOLIPASE C AND
USES THEREOF

Inventor: Rachel Meyers et al.
Application No.: Not yet assigned
Docket No.: 381552004800

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L F K D V I E T I N K Y A F I K N E Y P 410
CTC TTC AAA GAC GTC ATT GAA ACC ATC AAC AAA TAT GCC TTC ATC AAG AAT GAG TAC CCA 1230

V I L S I E N H C S V I Q Q K K M A Q Y 430
GTG ATC CTG TCC ATC GAA AAC CAC TGC AGT GTC ATC CAG CAG AAG AAA ATG GCC CAG TAT 1290

L T D I L G D K L D L S S V S S E D A T 450
CTG ACT GAC ATC CTT GGG GAC AAG CTG GAC CTG TCA TCA GTG AGC AGT GAA GAT GCC ACC 1350

T L P S P Q M L K G K I L V K G K K L P 470
ACA CTC CCC TCT CCA CAG ATG CTC AAG GGC AAG ATC CTC GTG AAG GGG AAG AAG CTC CCA 1410

A N I S E D A E E G E V S D E D S A D E 490
GCC AAC ATC AGC GAG GAT GCG GAG GAA GGC GAG GTG TCT GAT GAG GAC AGT GCT GAT GAG 1470

I D D D C K L L N G G D A S T N R K R V E 510
ATT GAC GAT GAC TGC AAG CTC CTC AAT GGG GAT GCA TCC ACC AAT CGA AAG CGT GTA GAA 1530

N T A K R K L D S L I K E S K I R D C E 530
AAC ACT GCT AAG AGG AAA CTG GAT TCC CTC ATC AAA GAG TCG AAG ATT CGG GAC TGT GAG 1590

D P N N F S V S T L S P S G K L G R K S 550
GAC CCC AAC AAC TTC TCC GTC TCC ACA CTG TCC CCA TCT GGA AAG CTC GGA CGC AAG AGC 1650

K A E E D V E S G E D A G G A S R R N G R 570
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L V V G S F S R R K K K G S K L K K A A 590
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S V A T H D I E M E A A S S W Q V S S F 650
TCC GTG GCC ACC CAC GAC ATA GAG ATG GAG GCG GCG TCC AGC TGG CAG GTG TCG TCC TTC 1950

S E T K A H Q I L Q Q K P A Q Y L R F N 670
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Q Q Q L S R I Y P S S Y R V D S S N Y N 690
CAG CAG CAG CTC TCC CGC ATC TAC CCC TCC TCC TAC CGT GTG GAC TCC AGC AAC TAC AAC 2070

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CCG CAG CCC TTC TGG AAC GCC GGC TGC CAA ATG GTT GCC CTG AAC TAC CAG TCA GAG GGG 2130

R M L Q L N R A K F S A N G G C G Y V L 730
CGG ATG CTG CAG CTG AAC CGA GCC AAG TTC AGC GCC AAC GGT GGC TGC GGC TAC GTA CTC 2190

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Q L K K Q L V L R I I S G Q Q L P K P R 770
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D S M L G D R G E I I D P F V E V E I I 790
GAC TCC ATG CTG GGG GAC CGT GGG GAG ATC ATC GAC CCC TTT GTG GAG GTG GAG ATC ATT 2370

G L P V D C S R E Q T R V V D D N G F N 810
GGG CTC CCT GTG GAC TGC AGC AGG GAG CAG ACC CGC GTG GTG GAC GAC AAC GGG TTC AAC 2430

P T W E E T L V F M V H M P E I A L V R 830
CCC ACC TGG GAG GAG ACC CTG GTT TTC ATG GTG CAC ATG CCG GAG ATC GCG CTG GTC CGC 2490

F L V W D H D P I G R D F I G Q R T L A 850
TTC CTC GTC TGG GAC CAC GAT CCC ATC GGG CGT GAC TTC ATT GGC CAG AGG ACG CTG GCC 2550

F S S M M P G Y R H V Y L E G M E E A S 870
TTC AGC AGC ATG ATG CCA GGC TAC AGA CAC GTG TAC CTA GAA GGG ATG GAA GAG GCC TCC 2610

FIGURE 1b

09927112"081001

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I F V H V A V S D I S G K V K Q A L G L 890
ATC TTC GTG CAT GTG GCT GTC AGT GAC ATC AGC GGT AAG GTC AAG CAG GCT CTG GGC CTA 2670

K G L F L R G P K P G S L D S H A A G R 910
AAA GGC CTC TTC CTC CGA GGC CCA AAG CCC GGC TCG CTG GAC AGT CAT GCT GCT GGG CGG 2730

P P A R P S V S Q R I L R R T A S A P T 930
CCC CCG GCC CGG CCC TCC GTT AGC CAG CGG ATC CTG CGG CGC ACG GCC AGC GCC CCG ACC 2790

K S Q K P G R R G F P E L V L G T R D T 950
AAG AGC CAG AAG CCG GGC CGC AGG GGC TTC CCG GAG CTG GTC CTG GGT ACA CGG GAC ACA 2850

G S K G V A D D V P P G P G P A P E A 970
GGC TCC AAG GGG GTG GCA GAC GAT GTG GTG CCC CCC GGG CCC GGA CCT GCT CCG GAA GCC 2910

P A Q E G P G S G P R G K A P A A V A 990
CCA GCC CAG GAG GGG CCC GGC AGC GGC AGC CCC CGA GGT AAG GCG CCA GCT GCG GTG GCA 2970

E K S P V R V R P P R V L D G P G P A G 1010
GAG AAG AGC CCT GTG CGA GTG CGG CCC CCG CGT GTC CTG GAC GGC CCC GGG CCT GCT GGG 3030

M A A T C M K C V V G S C A G V N T G G 1030
ATG GCC GCC ACA TGC ATG AAG TGT GTG GTG GGA TCC TGC GCC GGC GTG AAC ACC GGG GGC 3090

L Q R E R P P S P G P A S R Q A A I R Q 1050
CTG CAG AGG GAG CGG CCA CCC AGC CCG GGG CCT GCA AGC AGG CAG GCA GCC ATT CGC CAG 3150

Q P R A R A D S L G A P C C G L D P H A 1070
CAG CCC CGG GCC CGG GCT GAC TCA CTG GGG GCC CCC TGC TGT GGC CTG GAC CCT CAC GCT 3210

I P G R S R E A P K G P G A W R Q G P G 1090
ATC CCG GGG AGA AGC AGA GAG GCC CCC AAG GGT CCT GGG GCC TGG AGG CAG GGT CCA GGC 3270

G S G S M S S D S S S P D S P G I P E R 1110
GGT AGC GGC TCC ATG TCC TCG GAC TCC AGC AGC CCA GAC AGC CCG GGC ATC CCC GAA AGG 3330

S P R W P E G A C R Q P G A L Q G E M S 1130
TCC CCC CGC TGG CCT GAG GGT GCC TGC AGG CAA CCG GGG GCC CTG CAG GGA GAG ATG AGT 3390

A L F A Q K L E E I R S K S P M F S A G 1150
GCC TTG TTT GCT CAA AAG CTG GAG GAG ATC AGG AGT AAA TCC CCC ATG TTC TCC GCC GGT 3450

K P L L P C V V L P H A P G M A G P G S 1170
AAG CCC CTC TTG CCC TGC GTG GTC CTC CCG CAC GCC CCT GGC ATG GCT GGG CCT GGG TCA 3510

P A A A S A W T V S P R V L V L V A L Y 1190
CCT GCT GCT GCT TCT GCG TGG ACG GTG TCG CCT CGT GTG CTC GTG CTC GTG GCT CTG TAT 3570

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←SEQ ID NO:3↑

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GAAGCACCCTACTAGAAGGGTGTCTCCTTAGCCTGGAGGGAGGGACATACACGGAGCCCCCCCCACACCACCTGCCCC
TCCAGACCCCCCTGACCAAGCTTTCCTTCTGCCCCACCCACGCTTGCCCTCCGTAGTTAGGAAGTGAAGCGCGAGT
GACAGGTAACGGGGCCCCAGCCCCG

FIGURE 1c

Title: 32544, A NOVEL HUMAN PHOSPHOLIPASE C AND
USERS THEREOF

Inventors: Rachel Meyers et al.
Application No.: Not yet assigned
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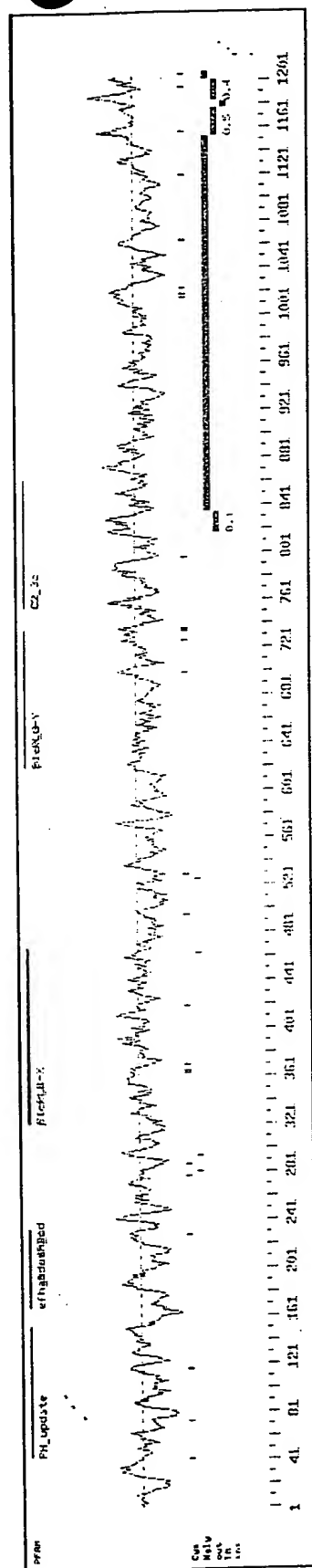


Fig. 2

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+++++v ++ ++ ++ +++++ +++++CF i ++++++l l +s+e +
32544 90 DSIqEVSEgRQsevfqrypdsfdpNCCFSIYHgSHreSLDLVSTSSEVA 139

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++WV+ +++++
32544 140 RTWVTGLRYLMA 151

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Fig. 3

```

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32544 169 WLKQTFDEADKNGDGSLSIGEVLQLLHKL 197

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Fig. 4a

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32544 205 RVKQMFREADTDHQGTGFGFEEFCAFYKMM 234

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Fig. 4b

```

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32544 323 DMTQPLSHYFITSSHNTYLVGDQLMSQSRVDMYAWVLQAGCRCVEVD 369

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32544 370 CWDG-PDGEPIVHHGYTLTSKILFKDVIETINKYAFI-KNEYPVILSIEN 417

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Hc++ qQ+kma+y+ +i+gd+L + + +t+ LPs+ +l+gKI
32544 418 HCSVI-QQKKMAQYLTDLGDKLDLSSVSSEDATT----LPSPQMLKGKI 462

LLknkk<-*
L+k+kk
32544 463 LVKGKK 468

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Fig. 5

FOOTNOTES 211 22660

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USES THEREOF

Inv: Rachel Meyers et al.
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32544 621 ALSDLVKYTKSV--ATHDIE-MEAASSWQVSSFSET--KAHQILQQK 662

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p + ++N+ qLsR+YP RvDSSN++Pq+fWnaGCQmVALN+Q+ +
32544 663 PAQYLRFNQQLSRIYPSSYRVDSSNYPNPQPFWNAGCQmVALNYQSEGRM 712

mqiNdGmFeyNggqPdGsfskGYLLKPeFlR<-*
+q+N ++F++Ngg +GY+LKP ++
32544 713 LQLNRAKFSANGG-----CGYVLKPGCMC 736

Fig. 6

*->LtVtvieArnLpkmDk.....vngrlsDPYVkvslldgdkdkkfkT SEQ ID NO:9
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32544 756 LVLRIISGQQLPKPRDsmldRGE-IIDPFVEVEIIGLPVDCSREQT 801

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32544 802 RVVDDN-GFNPTWE-ETLVFM-VHMPEIAL--VRFLVWDHDPiG-RDFiG 845

qvt<-*
q+t
32544 846 QRT 848

Fig. 7

Query: 883 KVKQALGLKGLFLRGPKPGSLDASHAAGRPPARPSVSQRILRRTASAPTKSQKPGRRGFPE 942
+VKQALGLKGLFLRGPKPGSLDASHAAGRPPARPSVSQRILRRTASAPTKSQKPGRRGFPE
Sbjct: 101 QVKQALGLKGLFLRGPKPGSLDASHAAGRPPARPSVSQRILRRTASAPTKSQKPGRRGFPE 160 SEQ ID NO:10

Query: 943 LVLGTRDTGSKXXXXXXXXXXXXXXXXXXXXXXXXXSGSPRGKAPAAVAEKSPVRVRPPRV 1002
LVLGTRDTGSK SGSPRGKAPAAVAEKSPVRVRPPRV
Sbjct: 161 LVLGTRDTGSKGVADDVVPVPPGPGPAPEAPAQEGPGSGSPRGKAPAAVAEKSPVRVRPPRV 220

Query: 1003 LDGPGPAGMAATCMKCVVGSCAGVNTGGLQRERPPSPGPASXXXXXXXXXXXXDSLGA 1062
LDGPGPAGMAATCMKCVVGSCAGVNTGGLQRERPPSPGPAS DSLGA
Sbjct: 221 LDGPGPAGMAATCMKCVVGSCAGVNTGGLQRERPPSPGPASQAIRQQPRARADSLGA 280

Query: 1063 CCGLDPHAIPGRSREAPKPGPAWRQXXXXXXXXXXXXXXXXXXXXIPERSPRWPEGACRQP 1122
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Sbjct: 281 CCGLDPHAIPGRSREAPKPGPAWRQPGGSGSMSSDSSSPDGIPERSPRWPEGACRQP 340

Query: 1123 GALQGEMSALFAQKLEEIRSKSPMFSAGKPLLPCVVLPHXXXXXXXXXXXXWTVSPR 1182
GALQGEMSALFAQKLEEIRSKSPMFSAGKPLLPCVVLPH WTVSPR
Sbjct: 341 GALQGEMSALFAQKLEEIRSKSPMFSAGKPLLPCVVLPHAPGMAGPGSPAAASAWTVSPR 400

Query: 1183 VLVLVALYPWHCLRGTLPLWLACGP 1207
VLVLVALYPWHCLRGTLPLWLACGP
Sbjct: 401 VLVLVALYPWHCLRGTLPLWLACGP 425

Fig. 8

09927112-081001

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Query: 307 SPAGDIFNPEHHHVHQDMTQPLSHYFITSSHNTYLVGDLMS-QSRVDMYAWVLQAGCRC 365
 SP ++F+PEH VHQM QPLSHYFI SSHNTYL G+QL S +S V+MY L GCRC
 Sbjct: 2 SPDCNVFDPEHKQVHQMNPQLSHYFINSSHNTYLTGNQLSSGESSVEMYRQALLKGCRC 61 SEQ ID NO:11

Query: 366 VEVDCWDGPDG--EPIVHHGYTLTSKILFKDVIETINKYAFIKNEYPVILSIENHCSVI- 422
 +E+DCWDG DG EPI+ HG+T+T++I FKD +E I ++AF+ +EYPVILS+ENHC
 Sbjct: 62 IELDCWDGKGDPEPIITHGHTMTTEISFKDCLEAIKEHAFVTSEYPVILSLENHCDSTP 121

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Fig. 9a

Query: 514 KRKLDLIKESKIRDCEDPNFVSSTLSPSGKLGRKSKAEEDVESGEDA 562
 KRK+ LIK K+++ + S K ++++EE+ E G DA
 Sbjct: 162 KRKI--LIKNNKLKEHSEEKE-----SEEKKTDEETESSEEDEMGSDA 202 SEQ ID NO:12

Fig. 9b

Query: 742 PNSEDPLPGQLKKQLVLR 759
 P E P P +LK+++++
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Fig. 9c

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 C+ MQ+G ++ K+R S R++ LD+ + W P S+K+ EK K I I+E+
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Query: 97 EGRQSEVFQRYPDGSF---DP-NCCFSIYHGSH--RESLDLVSTSSSEVARTWVTGLRYLM 150
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 RE D
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Fig. 10

00927112.081001

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Query: 174 FDEADKNGDGSLSIGEVLLQLLHKLNVNLPQRVKQMFREAD--TDDHQGT-LGFEEFCAF 230
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Query: 291 KSKGLLGIDGFTNY 304
+ G + IDGFT+Y
Sbjct: 122 RENGWMTIDGFTSY 135

Fig. 11

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Sbjct: 2 FSSLVPGYRHHVYLEGLTEASIFVHITINEIYGKNRQLQGLKGLFNKNPRHSSSENNS--H 59 SEQ ID NO:16

Query: 911 PPARPSVSQRILRRITASAPTKSQKPGRRGFPPELV 944
+ S+ RILRRITASAP K +K + GF E+V
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Fig. 12

099212.03100
FOOTED"CTZ660